

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- Sub  
a1
- (i) APPLICANT: Susan DYMECKI
- (ii) TITLE OF INVENTION: Use of Flp Recombinase in Mice
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
- (B) STREET: 1100 New York Avenue, N.W.
- (C) CITY: Washington
- (D) STATE: D.C.
- (E) COUNTRY: USA
- (F) ZIP: 20005-3918
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:
- 91

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGTGAAGT TCCTATTCCG AAGTTCTAT TCTCTAGAAA GTATAGGAAC

50

TTCCCTAGGA GATCTTCGAA GGCTCGAGC

79

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TAGCTACGTA GAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA 50  
GGAACCTCA 59

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAGGGAAGT TCCTATACTT TCTAGAGAAT AGGAACTTCG GAATAGGAAC 50  
TTCA 100

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGGTGAAGT TCCTATACTT TCTAGAGAAT AGGAACTTCG GAATAGGAAC 50  
TTCTACGTAG CTAGCTCGAG CCTTCGAAGA TCTC 84

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTAAGGTACC GGTGAAGTTC CTA 23

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

61 TTCACCCACC GGTGAAGTTC CTA 23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTACCGAGC TCAGCCACCA TGACTGCTCC AAAGAAGAAG CGTAAGGTAC 50  
CGGTGAAGTT CCTATTCCGA AGTTCCTATT CTCTAGAAAG TATAGGAACT 100  
TCACCGGTGG GTGAAGACCA GAAACAGCAC CTCGAACTGA GCCGCGATAT 150  
TGCCCAGCGT TTCAACGCGC TGTATGGCGA GATCGATCCC GTCGTTTTAC 200  
AACGTCGTGA C 211

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Ala Pro Lys Lys Lys Arg Lys Val Pro Val Lys Phe Leu  
1 5 10 15  
Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr Ser Pro Val  
20 25 30  
Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp Ile Ala  
35 40 45  
Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile Asp Pro Val Val Leu  
50 55 60  
Gln Arg Arg Asp

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Pro Lys Lys Lys Arg Lys Val  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Phe Leu Phe Arg Ser Ser Tyr Ser Leu Glu Ser Ile Gly Thr  
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Pro Val Gly Glu Asp Gln Lys Gln His Leu Glu Leu Ser Arg Asp  
1 5 10 15

Ile Ala Gln Arg Phe Asn Ala Leu Tyr Gly Glu Ile  
20 25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAAGTTCCTA TTC

13

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAAGTTCCTA TAC

13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTC

34

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAAGTTCCTA TTCCGAAGTT CCTATTCTCT AGAAAGTATA GGAAGTTC

48

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGCCACAAT TTGATATATT ATGTAAAACA CCACCTAAGG TGCTTGTTTCG TCAGTTTGTG 60  
GAAAGGTTTG AAAGACCTTC AGGTGAGAAA ATAGCATTAT GTGCTGCTGA ACTAACCTAT 120  
TTATGTTGGA TGATTACACA TAACGGAACA GCAATCAAGA GAGCCACATT CATGAGCTAT 180  
AATACTATCA TAAGCAATTC GCTGAGTTTG GATATTGTCA ACAAGTCACT GCAGTTTAAA 240

TACAAGACGC AAAAAGCAAC AATTCTGGAA GCCTCATTA AGAAATTGAT TCCTGCTTGG 300  
GAATTTACAA TTATTCCTTA CTATGGACAA AACATCAAT CTGATATCAC TGATATTGTA 360  
AGTAGTTTGC AATTACAGTT CGAATCATCG GAAGAAGCAG ATAAGGGAAA TAGCCACAGT 420  
AAAAAAATGC TTAAAGCACT TCTAAGTGAG GGTGAAAGCA TCTGGGAGAT CACTGAGAAA 480  
ATACTAAATT CGTTTGAGTA TACTTCGAGA TTTACAAAAA CAAAACTTT ATACCAATTC 540  
CTCTTCCTAG CTACTTTCAT CAATTGTGGA AGATTCAGCG ATATTAAGAA CGTTGATCCG 600  
AAATCATTTA AATTAGTCCA AAATAAGTAT CTGGGAGTAA TAATCCAGTG TTTAGTGACA 660  
GAGACAAAGA CAAGCGTTAG TAGGCACATA TACTTCTTTA GCGCAAGGGG TAGGATCGAT 720  
CCACTTGTAT ATTTGGATGA ATTTTGAGG AATTCTGAAC CAGTCCTAAA ACGAGTAAAT 780  
AGGACCGGCA ATTCTTCAAG CAACAAGCAG GAATACCAAT TATTAAAAGA TAACTTAGTC 840  
AGATCGTACA ACAAAGCTTT GAAGAAAAAT GCGCCTTATT CAATCTTTGC TATAAAAAAT 900  
GGCCCAAAAT CTCACATTGG AAGACATTTG ATGACCTCAT TTCTTTCAAT GAAGGGCCTA 960  
ACGGAGTTGA CTAATGTTGT GGGAAATTGG AGCGATAAGC GTGCTTCTGC CGTGGCCAGG 1020  
ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTTCTCGG 1080  
TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAAGGATGA GACTAATCCA 1140  
ATTGAGGAGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATACGATAC 1200  
CCCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTTCATC CTACATAAAT 1260  
AGACGCATAT AA 1272

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Pro	Gln	Phe	Asp	Ile	Leu	Cys	Lys	Thr	Pro	Pro	Lys	Val	Leu
1				5					10					15
Val	Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys
				20				25						30
Ile	Ala	Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile
				35				40						45
Thr	His	Asn	Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr
				50				55						60

Asn	Thr	Ile	Ile	Ser	Asn	Ser	Leu	Ser	Leu	Asp	Ile	Val	Asn	Lys	65	70	75
Ser	Leu	Gln	Phe	Lys	Tyr	Lys	Thr	Gln	Lys	Ala	Thr	Ile	Leu	Glu	80	85	90
Ala	Ser	Leu	Lys	Lys	Leu	Ile	Pro	Ala	Trp	Glu	Phe	Thr	Ile	Ile	95	100	105
Pro	Tyr	Tyr	Gly	Gln	Lys	His	Gln	Ser	Asp	Ile	Thr	Asp	Ile	Val	110	115	120
Ser	Ser	Leu	Gln	Leu	Gln	Phe	Glu	Ser	Ser	Glu	Glu	Ala	Asp	Lys	125	130	135
Gly	Asn	Ser	His	Ser	Lys	Lys	Met	Leu	Lys	Ala	Leu	Leu	Ser	Glu	140	145	150
Gly	Glu	Ser	Ile	Trp	Glu	Ile	Thr	Glu	Lys	Ile	Leu	Asn	Ser	Phe	155	160	165
Glu	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr	Leu	Tyr	Gln	Phe	170	175	180
Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gly	Arg	Phe	Ser	Asp	Ile	185	190	195
Lys	Asn	Val	Asp	Pro	Lys	Ser	Phe	Lys	Leu	Val	Gln	Asn	Lys	Tyr	200	205	210
Leu	Gly	Val	Ile	Ile	Gln	Cys	Leu	Val	Thr	Glu	Thr	Lys	Thr	Ser	215	220	225
Val	Ser	Arg	His	Ile	Tyr	Phe	Phe	Ser	Ala	Arg	Gly	Arg	Ile	Asp	230	235	240
Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val	245	250	255
Leu	Lys	Arg	Val	Asn	Arg	Thr	Gln	Asn	Ser	Ser	Ser	Asn	Lys	Gln	260	265	270
Glu	Tyr	Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys	275	280	285
Ala	Leu	Lys	Lys	Asn	Ala	Pro	Tyr	Ser	Ile	Phe	Ala	Ile	Lys	Asn	290	295	300
Gly	Pro	Lys	Ser	His	Ile	Gly	Arg	His	Leu	Met	Thr	Ser	Phe	Leu	305	310	315
Ser	Met	Lys	Gly	Leu	Thr	Glu	Leu	Thr	Asn	Val	Val	Gly	Asn	Trp	320	325	330
Ser	Asp	Lys	Arg	Ala	Ser	Ala	Val	Ala	Arg	Thr	Thr	Tyr	Thr	His	335	340	345
Gln	Ile	Thr	Ala	Ile	Pro	Asp	His	Tyr	Phe	Ala	Leu	Val	Ser	Arg	350	355	360
Tyr	Tyr	Ala	Tyr	Asp	Pro	Ile	Ser	Lys	Glu	Met	Ile	Ala	Leu	Lys	365	370	375

Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu  
380 385 390  
Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly  
395 400 405  
Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn  
410 415 420  
Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCCACAAT TTGATATATT ATGTAAACA CCACCTAAGG TGCTTGTTTCG TCAGTTTGTG 60  
GAAAGGTTTG AAAGACCTTC AGGTGAGAAA ATAGCATTAT GTGCTGCTGA ACTAACCTAT 120  
TTATGTTGGA TGATTACACA TAACGGAACA GCAATCAAGA GAGCCACATT CATGAGCTAT 180  
AATACTATCA TAAGCAATTC GCTGAGTTTC GATATTGTCA ACAAGTCACT GCAGTTTAAA 240  
TACAAGACGC AAAAAGCAAC AATTCTGGAA GCCTCATTAA AGAAATTGAT TCCTGCTTGG 300  
GAATTTACAA TTATTCCTTA CTATGGACAA AAACATCAAT CTGATATCAC TGATATTGTA 360  
AGTAGTTTGC AATTACAGTT CGAATCATCG GAAGAAGCAG ATAAGGGAAA TAGCCACAGT 420  
AAAAAAATGC TTAAAGCACT TCTAAGTGAG GGTGAAAGCA TCTGGGAGAT CACTGAGAAA 480  
ATACTAAATT CGTTTGAGTA TACTTCGAGA TTTACAAAA CAAAACTTT ATACCAATTC 540  
CTCTTCCTAG CTACTTTCAT CAATTGTGGA AGATTCAGCG ATATTAAGAA CGTTGATCCG 600  
AAATCATTTA AATTAGTCCA AAATAAGTAT CTGGGAGTAA TAATCCAGTG TTTAGTGACA 660  
GAGACAAAGA CAAGCGTTAG TAGGCACATA TACTTCTTTA GCGCAAGGGG TAGGATCGAT 720  
CCACTTGTAT ATTTGGATGA ATTTTGTAGG AATTCTGAAC CAGTCCTAAA ACGAGTAAAT 780  
AGGACCGGCA ATTCCTCAAG CAACAAGCAG GAATACCAAT TATTAAGA TAACCTAGTC 840  
AGATCGTACA ACAAAGCTTT GAAGAAAAAT GCGCCTTATT CAATCTTTGC TATAAAAAAT 900  
GGCCCAAAAT CTCACATTGG AAGACATTTG ATGACCTCAT TTCTTTCAAT GAAGGGCCTA 960  
ACGAGATTGA CTAATGTTGT GGGAAATTGG AGCGATAAGC GTGCTTCTGC CGTGGCCAGG 1020  
ACAACGTATA CTCATCAGAT AACAGCAATA CCTGATCACT ACTTCGCACT AGTTTCTCGG 1080

TACTATGCAT ATGATCCAAT ATCAAAGGAA ATGATAGCAT TGAAGGATGA GACTAATCCA 1140  
ATTGAGGAGT GGCAGCATAT AGAACAGCTA AAGGGTAGTG CTGAAGGAAG CATACGATAC 1200  
CCCGCATGGA ATGGGATAAT ATCACAGGAG GTACTAGACT ACCTTTCATC CTACATAAAT 1260  
AGACGCATAT AA 1272

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Pro	Gln	Phe	Asp	Ile	Leu	Cys	Lys	Thr	Pro	Pro	Lys	Val	Leu	1	5	10	15
Val	Arg	Gln	Phe	Val	Glu	Arg	Phe	Glu	Arg	Pro	Ser	Gly	Glu	Lys	20	25	30	
Ile	Ala	Leu	Cys	Ala	Ala	Glu	Leu	Thr	Tyr	Leu	Cys	Trp	Met	Ile	35	40	45	
Thr	His	Asn	Gly	Thr	Ala	Ile	Lys	Arg	Ala	Thr	Phe	Met	Ser	Tyr	50	55	60	
Asn	Thr	Ile	Ile	Ser	Asn	Ser	Leu	Ser	Phe	Asp	Ile	Val	Asn	Lys	65	70	75	
Ser	Leu	Gln	Phe	Lys	Tyr	Lys	Thr	Gln	Lys	Ala	Thr	Ile	Leu	Glu	80	85	90	
Ala	Ser	Leu	Lys	Lys	Leu	Ile	Pro	Ala	Trp	Glu	Phe	Thr	Ile	Ile	95	100	105	
Pro	Tyr	Tyr	Gly	Gln	Lys	His	Gln	Ser	Asp	Ile	Thr	Asp	Ile	Val	110	115	120	
Ser	Ser	Leu	Gln	Leu	Gln	Phe	Glu	Ser	Ser	Glu	Glu	Ala	Asp	Lys	125	130	135	
Gly	Asn	Ser	His	Ser	Lys	Lys	Met	Leu	Lys	Ala	Leu	Leu	Ser	Glu	140	145	150	
Gly	Glu	Ser	Ile	Trp	Glu	Ile	Thr	Glu	Lys	Ile	Leu	Asn	Ser	Phe	155	160	165	
Glu	Tyr	Thr	Ser	Arg	Phe	Thr	Lys	Thr	Lys	Thr	Leu	Tyr	Gln	Phe	170	175	180	
Leu	Phe	Leu	Ala	Thr	Phe	Ile	Asn	Cys	Gly	Arg	Phe	Ser	Asp	Ile	185	190	195	

Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn Lys Tyr  
 200 205 210  
 Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr Ser  
 215 220 225  
 Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp  
 230 235 240  
 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val  
 245 250 255  
 Leu Lys Arg Val Asn Arg Thr Gln Asn Ser Ser Ser Asn Lys Gln  
 260 265 270  
 Glu Tyr Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys  
 275 280 285  
 Ala Leu Lys Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn  
 290 295 300  
 Gly Pro Lys Ser His Ile Gly Arg His Leu Met Thr Ser Phe Leu  
 305 310 315  
 Ser Met Lys Gly Leu Thr Glu Leu Thr Asn Val Val Gly Asn Trp  
 320 325 330  
 Ser Asp Lys Arg Ala Ser Ala Val Ala Arg Thr Thr Tyr Thr His  
 335 340 345  
 Gln Ile Thr Ala Ile Pro Asp His Tyr Phe Ale Leu Val Ser Arg  
 350 355 360  
 Tyr Tyr Ala Tyr Asp Pro Ile Ser Lys Glu Met Ile Ala Leu Lys  
 365 370 375  
 Asp Glu Thr Asn Pro Ile Glu Glu Trp Gln His Ile Glu Gln Leu  
 380 385 390  
 Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr Pro Ala Trp Asn Gly  
 395 400 405  
 Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser Ser Tyr Ile Asn  
 410 415 420  
 Arg Arg Ile

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCCAACTG CAGCCCAAGC TTCC

24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGGATCGAT CCTACCCCTT GCG

23

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACTGCTCCA AAGAAGAAGC GTAAGG

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTATTACGC CAGCTGGCGA AAGG

24